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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/383,551

DATE: 11/10/1999
TIME: 15:51:47

Input Set: I383551.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1 <110> APPLICANT: Tamatani, Takuya
2   Tezuka, Katsunari
3 <120> TITLE OF INVENTION: CELL SURFACE MOLECULE MEDIATING CELL ADHESION AND SIGNAL
4 <130> FILE REFERENCE: 06501/039001
5 <140> CURRENT APPLICATION NUMBER: US/09/383,551
6 <141> CURRENT FILING DATE: 1999-08-26
7 <150> EARLIER APPLICATION NUMBER: WO PCT/JP98/00831
8 <151> EARLIER FILING DATE: 1998-02-21
9 <150> EARLIER APPLICATION NUMBER: JP 10/62217
10 <151> EARLIER FILING DATE: 1998-02-26
11 <150> EARLIER APPLICATION NUMBER: JP 9/62290
12 <151> EARLIER FILING DATE: 1997-02-27
13 <160> NUMBER OF SEQ ID NOS: 15
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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16 <211> LENGTH: 600
17 <212> TYPE: DNA
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25       1           5           10           15
26   gtt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg ttt ata      96
27   Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
28       20           25           30
29   ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac att gtc      144
30   Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
31       35           40           45
32   cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat      192
33   Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
34       50           55           60
35   ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag agt ctg      240
36   Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
37       65           70           75           80
38   aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt ttt cta      288
39   Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
40       85           90           95
41   tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac cta tca      336
42   Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
43       100          105          110
44   att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga tat ttg      384
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45      Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
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47      cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc      432
48      His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
49              130                      135                      140
50      ata gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt      480
51      Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
52      145                      150                      155                      160
53      att tgt tgg ctt aca aaa aag aag tat tca tcc agt gtg cac gac cct      528
54      Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
55              165                      170                      175
56      aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa aaa tct      576
57      Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
58              180                      185                      190
59      aga ctc aca gat gtg acc cta taa      600
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63      <211> LENGTH: 199
64      <212> TYPE: PRT
65      <213> ORGANISM: Homo sapiens
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69      Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
70              20                      25                      30
71      Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
72              35                      40                      45
73      Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
74              50                      55                      60
75      Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
76              65                      70                      75                      80
77      Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
78              85                      90                      95
79      Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
80              100                      105                      110
81      Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
82              115                      120                      125
83      His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
84              130                      135                      140
85      Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
86      145                      150                      155                      160
87      Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
88              165                      170                      175
89      Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
90              180                      185                      190
91      Arg Leu Thr Asp Val Thr Leu
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93      <210> SEQ ID NO 3
94      <211> LENGTH: 2610

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100     atttcacaac ggaggtgtac aaattttatg caaatatcct gacattgtcc agcaatttaa      180
101     aatgcagttg ctgaaagggg ggcaataact ctgcgatctc actaagacaa aaggaagtgg      240
102     aaacacagtg tccattaaga gtctgaaatt ctgccattct cagttatcca acaacagtgt      300
103     ctcttttttt ctatacaact tggaccattc tcatgccaac tattacttct gcaacctatc      360
104     aattttttgat cctcctcctt ttaaagtaac tcttacagga ggatatttgc atattttatga      420
105     atcacaactt tgttgccagc tgaagttctg gttaccataa ggatgtgcag cctttgttgt      480
106     agtctgcatt ttgggatgca tacttatttg ttggcttaca aaaaagaagt attcatccag      540
107     tgtgcacgac cctaacggtg aatacatggt catgagagca gtgaacacag ccaaaaaatc      600
108     tagactcaca gatgtgaccc tataatatgg aactctggca ccaggcatg aagcacgttg      660
109     gccagttttc ctcaacttga agtgcaagat tctcttattt ccgggaccac ggagagtctg      720
110     acttaactac atacatcttc tgctggtgtt ttgttcaatc tggaagaatg actgtatcag      780
111     tcaatgggga ttttaacaga ctgccctggg actgccgagt cctctcaaaa caaacaccct      840
112     cttgcaacca gctttggaga aagcccagct cctgtgtgct cactgggagt ggaatccctg      900
113     tctccacatc tgctcctagc agtgcacag ccagtaaaac aaacacattt acaagaaaaa      960
114     tgttttaaag atgccagggg tactgaatct gcaaagcaaa tgagcagcca aggaccagca      1020
115     tctgtccgca tttcactatc atactacctc ttctttctgt agggrrtgaga attcctcttt      1080
116     taatcagtca agggagatgc ttcaaagctg grgctatttt atttctgaga tgttgatgtg      1140
117     aactgtacat tagtacatac tcagtactct ccttcaattg ctgaacccca gttgaccatt      1200
118     ttaccaagac tttagatgct ttcttgtgcc ctcaattttc tttttaaaaa tacttctaca      1260
119     tgactgcttg acagcccaac agccactctc aatagagagc tatgtcttac attctttcct      1320
120     ctgctgctca atagttttat atatctatgc atacatatat acacacatat gtatataaaa      1380
121     ttcataatga atatatattgc ctatatcttc cctacaagaa tatttttgtc ccagaaagac      1440
122     atgttctttt ctcaaattca gttaaaatgg tttactttgt tcaagttagt ggtaggaaac      1500
123     attgcccgga attgaaagca aattttawwt attatcctat tttctaccat tatctatgtt      1560
124     ttcatggtgc tattaattac aagtttagtt ctttttgtag atcatattaa aattgcaaac      1620
125     aaaatcatct ttaatgggcc agcattctca tggggtagag cagaatattc atttagcctg      1680
126     aaagctgcag ttactatagg ttgctgtcag actataccca tgggtgctct gggcttgaca      1740
127     ggtcaaaatg gtcccatca gcctggagca gccctccaga cctgggtgga attccagggg      1800
128     tgagagactc ccctgagcca gaggccacta ggtattcttg ctcccagagg ctgaagtcac      1860
129     cctgggaatc acagtgggtc acctgcattc ataattccag gatctgtgaa gaggacatat      1920
130     gtgtcagggc acaattccct ctcataaaaa ccacacagcc tggaaattgg cctggccct      1980
131     tcaagatagc cttcttttaga atatgatttg gctagaaaga ttcttaataa tgtggaatat      2040
132     gattattctt agctggaata ttttctctac ttctgtctg catgccaag gcttctgaag      2100
133     cagccaatgt cgatgcaaca acatttgtaa ctttaggtaa actgggatta tgtttagtt      2160
134     taacattttg taactgtgtg cttatagttt acaagtgaga cccgatatgt cattatgcat      2220
135     acttatatta tcttaagcat gtgtaatgct ggatgtgtac agtacagtac wtaacttgta      2280
136     atttgaatct agtatggtgt tctgttttca gctgacttgg acaacctgac tggctttgca      2340
137     caggtgttcc ctgagttgtt tgcaggtttc tgtgtgtggg gtggggtatg gggaggagaa      2400
138     ccttcatggt ggcccacctg gcctggttgt ccaagctgtg cctcgacaca tctcatccc      2460
139     aagcatggga cacctcaaga tgaataataa ttcacaaaat ttctgtgaaa tcaaattccag      2520
140     ttttaagagg agccacttat caaagagatt ttaacagtag taagaaggca aagaataaac      2580
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143 <211> LENGTH: 2072
144 <212> TYPE: DNA

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152 1 5
153 gtc ttt gtc ttc tgc ttc cta atc aaa ctt tta aca gga gaa ctc aat 103
154 Val Phe Val Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly Glu Leu Asn
155 10 15 20
156 gac ttg gcc aat cac agg atg ttt tcg ttt cac gat gga ggt gta cag 151
157 Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly Gly Val Gln
158 25 30 35
159 att tct tgt aac tac cct gag act gtc cag cag tta aaa atg cag ttg 199
160 Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu
161 40 45 50 55
162 ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc 247
163 Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser
164 60 65 70
165 gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg 295
166 Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu
167 75 80 85
168 tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag 343
169 Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp Ser Ser Gln
170 90 95 100
171 ggc agc tac ttt tta tgc agc ctg tcg att ttc gac cca ccc cct ttt 391
172 Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe
173 105 110 115
174 caa gaa aag aac ctt agt gga gga tat ttg ctt att tat gaa tcc cag 439
175 Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln
176 120 125 130 135
177 ctt tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt 487
178 Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys Ala Ala Phe
179 140 145 150
180 gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa 535
181 Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp Phe Ala Lys
182 155 160 165
183 aag aag tac aga tcc agt gtg cac gac cct aat agc gag tac atg ttc 583
184 Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe
185 170 175 180
186 atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt atg acc 631
187 Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Met Thr
188 185 190 195
189 tca taatctggaa cacgggaacc catggaggaa ctacactgtc tagttcccct 684
190 Ser
191 200
192 gaaacttgaa tggagaaagt cttctatttt ctggaccaca gggcatctga cttgattaac 744
193 tactgatacc tccttttggk gttttgtttg tctggatcag tgactatcag tcaactcgaa 804
194 tttcagcaga ctgccctggg tttgctgagt ccttttaagg caaacccctt cttatagaag 864

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196      cctgcttcta gctatgcacc ggccagcaag acaaacatat ctccagcatt tttaaaaaaa      984
197      tgccagggta tgaatctgta aagtacacag gcagccattg accaccgtct gtccctcgttt    1044
198      tttcagattc tatttttttc catagagatc agcatttcct ctagaatcag acagtagagg    1104
199      gagatgcttc acaacagaag ctcttatgtt tctgagatgt tgatgaattc atgctttagt    1164
200      accaccatgt tctctaaciaa cttctatatt ccagctgac actgcttcag ggcttagatg    1224
201      cctgcttttg ccttcaagtc tccccctaaa gatactccca caggtctact tgggtggcctg    1284
202      cagccactct gaataggaag tttggtctac aattttcccc ctctgctgct caaaaaaaaaa    1344
203      aattagtaga tatgattttc ccatattctc cctgccaaag taattttttc cagcaaagac    1404
204      atctaaattc agttaatatg gtttactgtg ttgatattag tggcagtaaa cattttctcag    1464
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211      raattacaga ggggccaaga cagagttccc tcccctagaa actgtgcagc ctggaagtca    1884
212      gccctggcac tttaagatag ccttctttag aacatgagtt agttggtagt attctgacgt    1944
213      gtaaacagcc tatkgttgct cggagctgga ccattttctc cacttccctg tctgcatgcc    2004
214      taagacttct agagcagcca acgtatatgc aacattaaag aaaaaaaaaa aaaaaaaaaa    2064
215      aaaaaaaaaa                                2072
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226      1 5 10 15
227      ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca      96
228      Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
229      20 25 30
230      ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc      144
231      Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
232      35 40 45
233      cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa      192
234      Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
235      50 55 60
236      ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca      240
237      Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
238      65 70 75 80
239      atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta      288
240      Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
241      85 90 95
242      aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc      336
243      Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
244      100 105 110

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VERIFICATION SUMMARY
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Line	? Error/Warning	Original Text
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